PA   (GETH) GENENTECH INC.
XX
PI   Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
XX
DR   WPI; 2000-237871/20.
DR   P-PSDB; AAY99362.
XX
PT   New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT   PRO polypeptides, useful for screening of potential peptide or small
PT   molecule inhibitors of the relevant receptor/ligand interactions.
XX
PS   Claim 2; Fig 45; 773pp; English.
XX
CC   AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC   receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC   transmembrane and receptor PRO proteins can be used for screening of
CC   potential peptide or small molecule inhibitors of the relevant
CC   receptor/ligand interactions. The polypeptides and nucleotide sequences
CC   encoding then have various industrial applications, including uses as
CC   pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC   primers and hybridisation probes used in the isolation of the PRO
CC   polypeptides from the present invention
XX
SQ   Sequence 1989 BP; 340 A; 693 C; 586 G; 370 T; 0 U; 0 Other;

   Query Match   100.0%; Score 1989; DB 3; Length 1989;
   Best Local Similarity   100.0%; Pred. No. 0;
   Matches 1989; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1 GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCCATGGCGCTGCCATCCCGAATCCTG 60

Qy   61 CTTTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 CTTTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAG 120

Qy   121 ACGGACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 ACGGACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGC 180

Qy   181 CTGGCCGTCCGCCTGGAGGTCACCGACGGCCCCCCGGCCACCCCCGCCTACTGGGACGGC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 CTGGCCGTCCGCCTGGAGGTCACCGACGGCCCCCCGGCCACCCCCGCCTACTGGGACGGC 240

Qy   241 GAGAAGGAGGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 GAGAAGGAGGTGCTGGCGGTGGCGCGCGGCGCACCCGCGCTTCTGACCTGCGTGAACCGC 300

Qy   301 GGGCACGTGTGGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCACTGGGACCGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 GGGCACGTGTGGACCGACCGGCACGTGGAGGAGGCTCAACAGGTGGTGCACTGGGACCGG 360

Qy   361 CAGCCGCCCGGGGTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 CAGCCGCCCGGGGTCCCGCACGACCGCGCGGACCGCCTGCTGGACCTCTACGCGTCGGGC 420

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Qy    421  GAGCGCCGCGCCTACGGGCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCC  480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421  GAGCGCCGCGCCTACGGGCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCC  480

Qy    481  TTTGAGCGCGGTGACTTCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACC  540
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481  TTTGAGCGCGGTGACTTCTCACTGCGTATCGAGCCGCTGGAGGTCGCCGACGAGGGCACC  540

Qy    541  TACTCCTGCCACCTGCACCACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTG  600
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541  TACTCCTGCCACCTGCACCACCATTACTGTGGCCTGCACGAACGCCGCGTCTTCCACCTG  600

Qy    601  ACGGTCGCCGAACCCCACGCGGAGCCGCCCCCCCGGGGCTCTCCGGGCAACGGCTCCAGC  660
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601  ACGGTCGCCGAACCCCACGCGGAGCCGCCCCCCCGGGGCTCTCCGGGCAACGGCTCCAGC  660

Qy    661  CACAGCGGCGCCCCAGGCCCAGACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTC  720
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Db    661  CACAGCGGCGCCCCAGGCCCAGACCCCACACTGGCGCGCGGCCACAACGTCATCAATGTC  720

Qy    721  ATCGTCCCCGAGAGCCGAGCCCACTTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTG  780
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721  ATCGTCCCCGAGAGCCGAGCCCACTTCTTCCAGCAGCTGGGCTACGTGCTGGCCACGCTG  780

Qy    781  CTGCTCTTCATCCTGCTACTGGTCACTGTCCTCCTGGCCGCCCGCAGGCGCCGCGGAGGC  840
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781  CTGCTCTTCATCCTGCTACTGGTCACTGTCCTCCTGGCCGCCCGCAGGCGCCGCGGAGGC  840

Qy    841  TACGAATACTCGGACCAGAAGTCGGGAAAGTCAAAGGGGAAGGATGTTAACTTGGCGGAG  900
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    841  TACGAATACTCGGACCAGAAGTCGGGAAAGTCAAAGGGGAAGGATGTTAACTTGGCGGAG  900

Qy    901  TTCGCTGTGGCTGCAGGGGACCAGATGCTTTACAGGAGTGAGGACATCCAGCTAGATTAC  960
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Db    901  TTCGCTGTGGCTGCAGGGGACCAGATGCTTTACAGGAGTGAGGACATCCAGCTAGATTAC  960

Qy    961  AAAAACAACATCCTGAAGGAGAGGGCGGAGCTGGCCCACAGCCCCCTGCCTGCCAAGTAC  1020
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    961  AAAAACAACATCCTGAAGGAGAGGGCGGAGCTGGCCCACAGCCCCCTGCCTGCCAAGTAC  1020

Qy   1021  ATCGACCTAGACAAAGGGTTCCGGAAGGAGAACTGCAAATAGGGAGGCCCTGGGCTCCTG  1080
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1021  ATCGACCTAGACAAAGGGTTCCGGAAGGAGAACTGCAAATAGGGAGGCCCTGGGCTCCTG  1080

Qy   1081  GCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTCCTCGGGGCATCTCCTGATGCTCCG  1140
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1081  GCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTCCTCGGGGCATCTCCTGATGCTCCG  1140

Qy   1141  GGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCTGGAATTTGGCCTGGGCGTATGC  1200
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1141  GGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCTGGAATTTGGCCTGGGCGTATGC  1200

Qy   1201  AGAGGCCGCCTCCACACCCCTCCCCCAGGGGCTTGGTGGCAGCATAGCCCCCACCCCTGC  1260
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1201  AGAGGCCGCCTCCACACCCCTCCCCCAGGGGCTTGGTGGCAGCATAGCCCCCACCCCTGC  1260

Qy   1261  GGCCTTTGCTCACGGGTGGCCCTGCCCACCCCTGGCACAACCAAAATCCCACTGATGCCC  1320
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                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1261 GGCCTTTGCTCACGGGTGGCCCTGCCCACCCCTGGCACAACCAAAATCCCACTGATGCCC 1320

Qy     1321 ATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCCTGAAGACATTCCTGGAGG 1380
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Db     1321 ATCATGCCCTCAGACCCTTCTGGGCTCTGCCCGCTGGGGGCCTGAAGACATTCCTGGAGG 1380

Qy     1381 ACACTCCCATCAGAACCTGGCAGCCCCAAAACTGGGGTCAGCCTCAGGGCAGGAGTCCCA 1440
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1381 ACACTCCCATCAGAACCTGGCAGCCCCAAAACTGGGGTCAGCCTCAGGGCAGGAGTCCCA 1440

Qy     1441 CTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCCTGGAGGAGGACACTCCCAT 1500
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1441 CTCCTCCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCCTGGAGGAGGACACTCCCAT 1500

Qy     1501 CAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACTCCTCCTGGGG 1560
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Db     1501 CAGAACTTGGCAGCCTTGAAGTTGGGGTCAGCCTCGGCAGGAGTCCCACTCCTCCTGGGG 1560

Qy     1561 TGCTGCCTGCCACCAAGAGCTCCCCCACCTGTACCACCATGTGGGACTCCAGGCACCATC 1620
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Qy     1621 TGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTGCTTTGG 1680
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1621 TGTTCTCCCCAGGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTGCTTTGG 1680

Qy     1681 GCCACCTGGGGCTGCACCCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTGCTCT 1740
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Db     1681 GCCACCTGGGGCTGCACCCCCTGCCCTTTCTCTGCCCCATCCCTACCCTAGCCTTGCTCT 1740

Qy     1741 CAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTTGG 1800
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Db     1741 CAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCCTGACACCCCTCCCTTGG 1800

Qy     1801 ACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA 1860
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Db     1801 ACTCTGCCTGGGCTGGAGTCTAGGGCTGGGGCTACATTTGGCTTCTGTACTGGCTGAGGA 1860

Qy     1861 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCCACAT 1920
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1861 CAGGGGAGGGAGTGAAGTTGGTTTGGGGTGGCCTGTGTTGCCACTCTCAGCACCCCACAT 1920

Qy     1921 TTGCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAAA 1980
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Db     1921 TTGCATCTGCTGGTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAAA 1980

Qy     1981 AAAAAAAAA 1989
                |||||||||
Db     1981 AAAAAAAAA 1989
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